

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Bander, Neil H.

(ii) TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF  
PROSTATE CANCER

(iii) NUMBER OF SEQUENCES: 19

(iv) CORRESPONDENCE ADDRESS:

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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:  
(B) FILING DATE:  
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 60/016,976  
(B) FILING DATE: 06-MAY-1996

(viii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 06/022,125  
(B) FILING DATE: 18-JUL-1996

(ix) ATTORNEY/AGENT INFORMATION:

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(C) REFERENCE/DOCKET NUMBER: 19603/1172

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 391 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TCTCCTGTCA	GGAAC TGCAG	GTGTCCTCTC	TGAGGTCCAG	CTGCAACAGT	CTGGACCTGA	60
ACTGGTGAAG	CCTGGGACTT	CAGTGAGGAT	ATCCTGCAAG	ACTTCTGGAT	ACACATT CAC	120
TGAATATAACC	ATACACTGGG	TGAAGCAGAG	CCATGGAAAG	AGCCTTGAGT	GGATTGGAAA	180
CATCAATCCT	AACAATGGTG	GTACCA CCTA	CAATCAGAAG	TTCGAGGACA	AGGCCACATT	240
GA C T G T A G A C	AAGTCCTCCA	GTACAGCCTA	CATGGAGCTC	CGCAGCCTAA	CATCTGAGGA	300
TTCTGCAGTC	TATTATTGTG	CAGCTGGTTG	GAAC TTTGAC	TACTGGGGCC	AAGGCACCAC	360
TCTCACAGTC	TCCTCAGCCA	AAACGACACC	C			391

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 391 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GGGTGTCGTT	TTGGCTGAGG	AGACTGTGAG	AGTGGTGCCT	TGGCCCCAGT	AGTC A AAGTT	60
CCAACCAGCT	GCACAATAAT	AGACTGCAGA	ATCCTCAGAT	GTTAGGCTGC	GGAGCTCCAT	120
GTAGGCTGTA	CTGGAGGACT	TGTCTACAGT	CAATGTGGCC	TTGTCCCTCGA	ACTTCTGATT	180
GTAGGTGGTA	CCACCATTGT	TAGGATTGAT	GTTTCCAATC	CACTCAAGGC	TCTTCCATG	240
GCTCTGCTTC	ACCCAGTGT A	TGGTATATTC	AGTGAATGTG	TATCCAGAAG	TCTTGCAGGA	300
TATCCTCACT	GAAGTCCCAG	GCTTCACCA G	TTCAGGTCCA	GACTGTTGCA	GCTGGACCTC	360
AGAGAGGACA	CCTGCAGTTC	CTAGCAGGAG	A			391

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Ser	Pro	Val	Arg	Asn	Cys	Arg	Cys	Pro	Leu	Gly	Pro	Ala	Ala	Thr	Val
1				5					10					15	
Trp	Thr	Thr	Gly	Glu	Ala	Trp	Asp	Phe	Ser	Glu	Asp	Ile	Leu	Gln	Asp
	20					25						30			
Phe	Trp	Ile	His	Ile	His	Ile	Tyr	His	Thr	Leu	Gly	Glu	Ala	Glu	Pro
	35					40						45			
Trp	Lys	Glu	Pro	Val	Asp	Trp	Lys	His	Gln	Ser	Gln	Trp	Trp	Tyr	His
	50				55							60			
Leu	Gln	Ser	Glu	Val	Arg	Gly	Gln	Gly	His	Ile	Asp	Cys	Arg	Gln	Val
	65				70				75					80	
Leu	Gln	Tyr	Ser	Leu	His	Gly	Ala	Pro	Gln	Pro	Asn	Ile	Gly	Phe	Cys
		85				90								95	
Ser	Leu	Leu	Leu	Cys	Ser	Trp	Leu	Glu	Leu	Leu	Gly	Pro	Arg	His	
					100			105					110		
His	Ser	His	Ser	Leu	Leu	Ser	Gln	Asn	Asp	Thr					
					115			120							

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Leu	Leu	Ser	Gly	Thr	Ala	Gly	Val	Leu	Ser	Glu	Val	Gln	Leu	Gln	Gln
1				5				10				15			
Ser	Gly	Pro	Glu	Leu	Val	Lys	Pro	Gly	Thr	Ser	Val	Arg	Ile	Ser	Cys
	20				25							30			
Lys	Thr	Ser	Gly	Tyr	Thr	Phe	Thr	Glu	Tyr	Thr	Ile	His	Trp	Val	Lys
	35					40						45			

Gln Ser His Gly Lys Ser Leu Glu Trp Ile Gly Asn Ile Asn Pro Asn  
50 55 60

Asn Gly Gly Thr Thr Tyr Asn Gln Lys Phe Glu Asp Lys Ala Thr Leu  
65 70 75 80

Thr Val Asp Lys Ser Ser Thr Ala Tyr Met Glu Leu Arg Ser Leu  
85 90 95

Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Ala Gly Trp Asn Phe  
100 105 110

Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Ala Lys Thr  
115 120 125

Thr Pro  
130

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Leu Ser Cys Gln Glu Leu Gln Val Ser Ser Leu Arg Ser Ser Cys Asn  
1 5 10 15

Ser Leu Asp Leu Asn Trp Ser Leu Gly Leu Gln Gly Tyr Pro Ala Arg  
20 25 30

Leu Leu Asp Thr His Ser Leu Asn Ile Pro Tyr Thr Gly Ser Arg Ala  
35 40 45

Met Glu Arg Ala Leu Ser Gly Leu Glu Thr Ser Ile Leu Thr Met Val  
50 55 60

Val Pro Pro Thr Ile Arg Ser Ser Arg Thr Arg Pro His Leu Thr Ser  
65 70 75 80

Pro Pro Val Gln Pro Thr Trp Ser Ser Ala Ala His Leu Arg Ile Leu  
85 90 95

Gln Ser Ile Ile Val Gln Leu Val Gly Thr Leu Thr Thr Gly Ala Lys  
100 105 110

Ala Pro Leu Ser Gln Pro Ser Gln Pro Lys Arg His Pro  
115 120 125

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GAGGTCCAGC TGCAACAGTC TGGACCTGAA CTGGTGAAGC CTGGGACTTC AGTGAGGATA	60
TCCTGCAAGA CTTCTGGATA CACATTCACT GAATATACCA TACACTGGGT GAAGCAGAGC	120
CATGGAAAGA GCCTTGAGTG GATTGGAAAC ATCAATCCTA ACAATGGTGG TACCACCTAC	180
AATCAGAAGT TCGAGGACAA GGCCACATTG ACTGTAGACA AGTCCTCCAG TACAGCCTAC	240
ATGGAGCTCC GCAGCCTAAC ATCTGAGGAT TCTGCAGTCT ATTATTGTGC AGCTGGTTGG	300
AACTTTGACT ACTGGGGCCA AGGCACCACT CTCACAGTCT CCTCA	345

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TGAGGAGACT GTGAGAGTGG TGCCTGGCC CCAGTAGTCA AAGTTCCAAC CAGCTGCACA	60
ATAATAGACT GCAGAACCT CAGATGTTAG GCTGCGGAGC TCCATGTAGG CTGTACTGGA	120
GGACTTGTCT ACAGTCAATG TGGCCTTGTC CTCGAACCTTC TGATTGTAGG TGGTACCAACC	180
ATTGTTAGGA TTGATGTTTC CAATCCACTC AAGGCTCTT CCATGGCTCT GCTTCACCCA	240
GTGTATGGTA TATTCAAGTGA ATGTGTATCC AGAAAGTCTTG CAGGATATCC TCACTGAAGT	300
CCCAGGCTTC ACCAGTTCAAG GTCCAGACTG TTGCAGCTGG ACCTC	345

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Thr  
1 5 10 15

Ser Val Arg Ile Ser Cys Lys Thr Ser Gly Tyr Thr Phe Thr Glu Tyr  
20 25 30

Thr Ile His Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile  
35 40 45

Gly Asn Ile Asn Pro Asn Asn Gly Gly Thr Thr Tyr Asn Gln Lys Phe  
50 55 60

Glu Asp Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr  
65 70 75 80

Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys  
85 90 95

Ala Ala Gly Trp Asn Phe Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr  
100 105 110

Val Ser Ser  
115

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TTATATGGAG CTGATGGAA CATTGTAATG ACCCAATCTC CCAAATCCAT GTCCATGTCA	60
GTAGGAGAGA GGGTCACCTT GACCTGCAAG GCCAGTGAGA ATGTGGTTAC TTATGTTCC	120
TGGTATCAAC AGAAACCAGA GCAGTCTCCT AAACTGCTGA TATACGGGGC ATCCAACCGG	180
TACACTGGGG TCCCCGATCG CTTCACAGGC AGTGGATCTG CAACAGATTT CACTCTGACC	240

ATCAGCAGTG TGCAGGCTGA AGACCTTGCA GATTATCACT GTGGACAGGG TTACAGCTAT	300
CCGTACACGT TCGGAGGGGG GACCAAGCTG GAAATAAAAC GGGCTGATGC TGCACCAACT	360
GTA	363

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TACAGTTGGT GCAGCATCAG CCCGTTTAT TTCCAGCTTG GTCCCCCTC CGAACGTGTA	60
CGGATAGCTG TAACCCTGTC CACAGTGATA ATCTGCAAGG TCTTCAGCCT GCACACTGCT	120
GATGGTCAGA GTGAAATCTG TTGCAGATCC ACTGCCTGTG AAGCGATCGG GGACCCCAGT	180
GTACCGGTTG GATGCCCGT ATATCAGCAG TTTAGGAGAC TGCTCTGGTT TCTGTTGATA	240
CCAGGAAACA TAAGTAACCA CATTCTCACT GGCCCTGCAG GTCAAGGTGA CCCTCTCTCC	300
TACTGACATG GACATGGATT TGGGAGATTG GGTTCATTACA ATGTTCCCAT CAGCTCCATA	360
TAA	363

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Leu Tyr Gly Ala Asp Gly Asn Ile Val Met Thr Gln Ser Pro Lys Ser			
1	5	10	15
Met Ser Met Ser Val Gly Glu Arg Val Thr Leu Thr Cys Lys Ala Ser			
20	25	30	
Glu Asn Val Val Thr Tyr Val Ser Trp Tyr Gln Gln Lys Pro Glu Gln			
35	40	45	
Ser Pro Lys Leu Leu Ile Tyr Gly Ala Ser Asn Arg Tyr Thr Gly Val			
50	55	60	

Pro Asp Arg Phe Thr Gly Ser Gly Ser Ala Thr Asp Phe Thr Leu Thr  
65 70 75 80

Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Asp Tyr His Cys Gly Gln  
85 90 95

Gly Tyr Ser Tyr Pro Tyr Thr Phe Gly Gly Thr Lys Leu Glu Ile  
100 105 110

Lys Arg Ala Asp Ala Ala Pro Thr Val  
115 120

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Tyr Met Glu Leu Met Gly Thr Leu Pro Asn Leu Pro Asn Pro Cys Pro  
1 5 10 15

Cys Gln Glu Arg Gly Ser Pro Pro Ala Arg Pro Val Arg Met Trp Leu  
20 25 30

Leu Met Phe Pro Gly Ile Asn Arg Asn Gln Ser Ser Leu Leu Asn Cys  
35 40 45

Tyr Thr Gly His Pro Thr Gly Thr Leu Gly Ser Pro Ile Ala Ser Gln  
50 55 60

Ala Val Asp Leu Gln Gln Ile Ser Leu Pro Ser Ala Val Cys Arg Leu  
65 70 75 80

Lys Thr Leu Gln Ile Ile Thr Val Asp Arg Val Thr Ala Ile Arg Thr  
85 90 95

Arg Ser Glu Gly Gly Pro Ser Trp Lys Asn Gly Leu Met Leu His Gln  
100 105 110

Leu Tyr

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Ile Ile Trp Ser Trp Glu His Cys Asn Asp Pro Ile Ser Gln Ile His  
1 5 10 15

Val His Val Ser Arg Arg Glu Gly His Leu Asp Leu Gln Gly Gln Glu  
20 25 30

Cys Gly Tyr Leu Cys Phe Leu Val Ser Thr Glu Thr Arg Ala Val Ser  
35 40 45

Thr Ala Asp Ile Arg Gly Ile Gln Pro Val His Trp Gly Pro Arg Ser  
50 55 60

Leu His Arg Gln Trp Ile Cys Asn Arg Phe His Ser Asp His Gln Gln  
65 70 75 80

Cys Ala Gly Arg Pro Cys Arg Leu Ser Leu Trp Thr Gly Leu Gln Leu  
85 90 95

Ser Val His Val Arg Arg Gly Asp Gln Ala Gly Asn Lys Thr Gly Cys  
100 105 110

Cys Thr Asn Cys  
115

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

AACATTGTAA TGACCCAATC TCCCAAATCC ATGTCCATGT CAGTAGGAGA GAGGGTCACC	60
TTGACCTGCA AGGCCAGTGA GAATGTGGTT ACTTATGTTT CCTGGTATCA ACAGAAACCA	120
GAGCAGTCTC CTAAACTGCT GATATACGGG GCATCCAACC GGTACACTGG GGTCCCCGAT	180
CGCTTCACAG GCAGTGGATC TGCAACAGAT TTCACTCTGA CCATCAGCAG TGTGCAGGCT	240
GAAGACCTTG CAGATTATCA CTGTGGACAG GGTTACAGCT ATCCGTACAC GTTCGGAGGG	300
GGGACCAAGC TGGAAATAAA A	321

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TTTTATTC	AGCTTGGTCC	CCCCTCCGAA	CGTGTACCGA	TAGCTGTAAC	CCTGTCCACA	60
GTGATAATCT	GCAAGGTCTT	CAGCCTGCAC	ACTGCTGATG	GTCAGAGTGA	AATCTGTTGC	120
AGATCCACTG	CCTGTGAAGC	GATCGGGGAC	CCCAGTGTAC	CGGTTGGATG	CCCCGTATAT	180
CAGCAGTTA	GGAGACTGCT	CTGGTTCTG	TTGATACCAG	GAAACATAAG	TAACCACATT	240
CTCACTGGCC	TTGCAGGTCA	AGGTGACCCCT	CTCTCCTACT	GACATGGACA	TGGATTTGGG	300
AGATTGGGTC	ATTACAATGT	T				321

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Asn	Ile	Val	Met	Thr	Gln	Ser	Pro	Lys	Ser	Met	Ser	Met	Ser	Val	Gly
1					5			10						15	
Glu	Arg	Val	Thr	Leu	Thr	Cys	Lys	Ala	Ser	Glù	Asn	Val	Val	Thr	Tyr
				20				25				30			
Val	Ser	Trp	Tyr	Gln	Gln	Lys	Pro	Glu	Gln	Ser	Pro	Lys	Leu	Leu	Ile
				35			40					45			
Tyr	Gly	Ala	Ser	Asn	Arg	Tyr	Thr	Gly	Val	Pro	Asp	Arg	Phe	Thr	Gly
				50			55				60				
Ser	Gly	Ser	Ala	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Val	Gln	Ala
				65			70			75			80		
Glu	Asp	Leu	Ala	Asp	Tyr	His	Cys	Gly	Gln	Gly	Tyr	Ser	Tyr	Pro	Tyr
				85				90				95			
Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys					
					100			105							

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 321 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GACATTGTGA	TGACCCAGTC	TCACAAATTC	ATGTCCACAT	CAGTAGGAGA	CAGGGTCAGC	60
ATCATCTGTA	AGGCCAGTCA	AGATGTGGGT	ACTGCTGTAG	ACTGGTATCA	ACAGAAACCA	120
GGACAATCTC	CTAAACTACT	GATTTATTGG	GCATCCACTC	GGCACACTGG	AGTCCCTGAT	180
CGCTTCACAG	GCAGTGGATC	TGGGACAGAC	TTCACTCTCA	CCATTACTAA	TGTTCAAGTCT	240
GAAGACTTGG	CAGATTATTT	CTGTCAGCAA	TATAACAGCT	ATCCTCTCAC	GTTCGGTGCT	300
GGGACCATGC	TGGACCTGAA	A				321

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 321 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TTTCAGGTCC	AGCATGGTCC	CAGCACCGAA	CGTGAGAGGA	TAGCTGTTAT	ATTGCTGACA	60
GAAATAATCT	GCCAAGTCTT	CAGACTGAAC	ATTAGTAATG	GTGAGAGTGA	AGTCTGTCCC	120
AGATCCACTG	CCTGTGAAGC	GATCAGGGAC	TCCAGTGTGC	CGAGTGGATG	CCCAATAAAT	180
CAGTAGTTA	GGAGATTGTC	CTGGTTCTG	TTGATACCAAG	TCTACAGCAG	TACCCACATC	240
TTGACTGGCC	TTACAGATGA	TGCTGACCCCT	GTCTCCTACT	GATGTGGACA	TGAATTTGTG	300
AGACTGGGTC	ATCACAATGT	C				321

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 107 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Asp	Ile	Val	Met	Thr	Gln	Ser	His	Lys	Phe	Met	Ser	Thr	Ser	Val	Gly
1					5				10					15	
Asp	Arg	Val	Ser	Ile	Ile	Cys	Lys	Ala	Ser	Gln	Asp	Val	Gly	Thr	Ala
	20						25						30		
Val	Asp	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ser	Pro	Lys	Leu	Leu	Ile
		35				40						45			
Tyr	Trp	Ala	Ser	Thr	Arg	His	Thr	Gly	Val	Pro	Asp	Arg	Phe	Thr	Gly
		50				55					60				
Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Thr	Asn	Val	Gln	Ser
	65				70				75				80		
Glu	Asp	Leu	Ala	Asp	Tyr	Phe	Cys	Gln	Gln	Tyr	Asn	Ser	Tyr	Pro	Leu
			85				90						95		
Thr	Phe	Gly	Ala	Gly	Thr	Met	Leu	Asp	Leu	Lys					
					100				105						